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# ADF

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## *FINAL REPORT*

20010098

# IMPLEMENTATION OF MARKER-ASSISTED SELECTION FOR LODGING RESISTANCE IN PEA BREEDING

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# FINAL REPORT

**"Implementation of marker-assisted selection for lodging resistance in pea breeding"**

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**Project: 20010098**

## (a) Abstract/Summary

Lodging resistance is a key criterion in pea breeding programs. Traditionally, breeders apply selection for lodging resistance in the $F_3$ or later generations. Molecular markers linked to two quantitative trait loci (QTL) for lodging resistance in pea have been identified. The objective of this research was to evaluate the effectiveness of marker-assisted selection (MAS) for lodging resistance in early generations of pea breeding. $F_3$ families derived from MAS in $F_1$ and $F_2$ generations and $F_3$ families from unselected populations were evaluated for lodging reaction at Canada-Saskatchewan Irrigation Diversification Centre (CSIDC), Outlook, SK, in the summer of 2003. Using markers linked to each locus, we were able to differentiate the individuals carrying different loci for lodging resistance. The most lodging resistant $F_3$ families were obtained from MAS with the combination of the presence of A001 marker and the absence of A004 marker. This combination also captured a higher proportion of lodging resistant $F_3$ families compared to phenotypic selection. These results coupled with the lower cost of MAS than phenotypic selection support the potential use of the markers for MAS in early generations of pea breeding and savings to the breeding program should be realized. The results of analysis using A001, A002 and A004 markers on 53 commercial pea varieties indicated the broad applicability of these markers.

## (b) Executive Summary

Development of improved cultivars for pulse growers is a critical component in enhancing the competitiveness of the field pea crop in western Canada. Lodging resistance is a key criterion in pea breeding programs. Traditionally, breeders apply selection for lodging resistance in the $F_3$ or later generations. Thus, a large number of inferior lines are maintained for several years before being discarded. Implementation of selection using molecular markers for lodging resistance at earlier generations ($F_1$ or $F_2$), therefore, will significantly enhance the efficiency of the pea breeding process. Markers associated with two QTL for lodging resistance in pea have been identified. These markers, namely A001, A002 and A004, were identified in a pea inbred population derived from a cross between MP1401 (lodging susceptible) and Carneval (lodging resistant). The objective of this research project was to evaluate the effectiveness of MAS for lodging resistance using different combinations of these markers in $F_1$ and $F_2$ generations of pea. Ten $F_2$ populations consisting of 869 plants derived from single

crosses, and another 10 populations consisting of 314 $F_1$ plants derived from three-way and double crosses were scored for the presence or absence of the markers associated with lodging resistance. In summer of 2003, a total of 1340 $F_3$ families derived from MAS in $F_1$ and $F_2$ generations and 318 $F_3$ families from three unselected populations were evaluated for lodging reaction at CSIDC, Outlook, SK.

The results of the study confirmed the presence of at least two loci associated with lodging resistance in pea. Using markers linked to each locus, we were able to differentiate the individuals carrying different loci for lodging resistance. The lowest lodging scores derived from single, three way and double cross populations were obtained from the combination of A001(+)A004(-). A higher proportion of lodging resistant $F_3$ families was also obtained from this marker combination as compared to conventional phenotypic selection. The current cost estimate demonstrated a much cheaper cost for MAS ($2.80/sample) than for phenotypic selection for lodging resistance at the $F_3$ generation using microplots ($10/microplot). Thus, the current research demonstrated that A001 and A004 are useful for MAS for lodging resistance in early generations of pea breeding. Our survey using these markers on 53 commercial pea varieties with relatively different genetic backgrounds demonstrated that the markers correspond well with the lodging reaction of these varieties indicating that the markers may have broad applicability.

**(c) Technical Report**

**Background**

To enhance export and domestic markets for Canadian pea production, the cost of production must remain competitive and the crop must retain its high quality. Development of new pea cultivars for Canadian pulse growers is a critical component in the effort to ensure that these objectives are achieved. Lodging resistance is a key criterion in pea breeding programs. Traditionally, breeders apply selection for lodging resistance in the $F_3$ or later generations, since it is difficult to assess lodging resistance on a single plant basis in $F_1$ or $F_2$ generations. The Crop Development Centre, University of Saskatchewan (CDC) pulse breeding program utilizes an $F_2$-derived family breeding method. Selection for simply inherited traits, such as resistance to powdery mildew and semileafless leaf type is conducted in the heterozygous $F_1$ or $F_2$ generations. This technique, however, does not allow adequate evaluation for more complex traits such as lodging resistance until $F_3$ or later generations. Approximately 10,000 $F_3$ microplot families are screened in the field annually in the CDC program. A large number of these families are discarded because of susceptibility to lodging. Implementation of selection using molecular markers for lodging resistance at earlier generations ($F_1$ or $F_2$), therefore, will significantly enhance the efficiency of the pea breeding process. It will enrich the $F_3$ and subsequent nurseries for lodging resistance, and allow more intense selection for other traits of interest such as mycosphaerella blight resistance and early maturity. However, before this approach can be integrated into an applied breeding program on a routine basis, an evaluation of its efficiency as compared to conventional methods was needed.

A major advance in genetic research over the past few years has been the development of lower cost molecular markers that can be used in marker-assisted selection in breeding programs. Molecular markers are pieces of genetic code that are associated with traits important in crop varieties. Breeders usually select for traits that are observed under field conditions. However, these traits can be skewed depending on the influence of the field season and growing conditions. The presence or absence of genetic markers is stable regardless of the environment. Thus, a strong association of a marker with a trait will allow the breeder to more effectively select for the trait regardless of the environmental conditions. Although associations between molecular markers and traits have been established for a number of crops, few results from MAS in applied plant breeding exist.

Markers associated with QTL for lodging resistance in pea have been identified by the authors in a project supported by the Western Grains Research Foundation (Tar'an et al., 2003). Three AFLP markers, namely A001, A002 and A004, linked to lodging resistance were identified in a pea-inbred population derived from a cross between MP1401 (lodging susceptible) and Carneval (lodging resistant). These markers have been converted into sequence characterized amplified region (SCAR) markers to simplify the analysis. The A001 and A002 markers were linked in coupling phase with the locus for lodging resistance, while the A004 marker was linked in repulsion phase. Our final analysis revealed that A001 and A002 were linked at a distance of 5.5 cM on linkage group III (Tar'an et al. 2003); therefore, for MAS we mainly focus on the use of A001 and A004 markers. Preliminary analysis indicated that the A001 marker is present in 10 pea varieties with known lodging resistance and absent in six out of nine lodging susceptible varieties. These results suggested that the marker has broad applicability for selecting for lodging resistance in pea. We are intending to integrate the information from this research into the CDC and AAFC pea breeding programs. The recent five-year review of the CDC recommended that MAS technical assistance be provided to the CDC breeding programs. However, before this approach can be utilized in a routine manner in field pea breeding, an evaluation of its efficiency as compared to conventional selection is needed.

## Objectives

The overall objective of this research was to evaluate the effectiveness and efficiency of MAS for lodging resistance in early generations of pea breeding. The specific objectives were: 1) to examine the lodging reaction of the $F_3$ families selected based on marker genotype in the $F_2$ generation derived from single crosses, 2) to examine the lodging reaction of the $F_3$ families selected based on marker genotype in the $F_1$and $F_2$ generations derived from three way and double crosses, 3) to examine the lodging reaction of unselected $F_3$ families, and 4) to compare the performance of $F_3$ families derived from marker-based selection for lodging resistance with the non-selected lines (conventional selection). This study provides pea breeders with a new tool for quickly evaluating lodging resistance in their populations, thus, increasing the frequency of genes associated with lodging resistance in breeding populations.

To reach these goals, we slightly modified the procedures of MAS using A001 and A004 markers based on the results of the latest QTL analysis on the original mapping population. Three sets of populations, two for MAS and one for phenotypic/conventional selection, were developed:

A. MAS on the $F_2$ populations: The $F_2$ plants from 10 different populations were grouped into four categories (T1 – T4) based on the combination scores of A001 and A004 markers [T1 = A001(+)A004(+); T2 = A001(+)A004(-); T3 = A001(-) A004(+) and T4 = A001(-)A004(-); Fig. 1]
B. MAS on $F_1$ generation: The heterozygous $F_1$ plants derived from three way and double crosses were scored using A001 and A004 markers followed by the same analysis on the $F_2$ plants. The $F_1$ and $F_2$ plants from these crosses were also grouped into four categories (T1, T2, T3 and T4; Fig. 2). Ten populations derived from three way and double crosses were developed. Three of these populations also segregated for the A002 marker.
C. Conventional/phenotypic selection at the $F_3$ generation.

## Materials and Methods

**Parents and population development**: The lodging reaction and marker scores of the varieties used in crosses for this research project are summarized (Table 1). Ten lodging resistant varieties were crossed to lodging susceptible parent, Carrera, to generate 10 single cross populations. The $F_1$ progeny from these single crosses were then used in three-way crosses to another lodging susceptible variety (CDC April, CDC Vienna or CDC Minuet), or used in double crosses. The crosses and the number of $F_1$, $F_2$ and $F_3$ families from each cross/population are described in Table 2.

Table 1. Lodging score and marker genotype of varieties used in single crosses.

| No. | Cultivars | Lodging reaction | Marker score A001 | A002 | A004 |
|---|---|---|---|---|---|
| 1 | DS Dominator | G | + | + | - |
| 2 | Carneval | G | + | + | - |
| 3 | Toledo | G | + | - | - |
| 4 | Nitouche | G | + | - | + |
| 5 | Swing | G | + | + | - |
| 6 | DS Admiral | G | + | + | - |
| 7 | Integra | G | + | + | - |
| 8 | Miami | G | + | + | - |
| 9 | Majoret | G | + | + | - |
| 10 | MP1101 | G | + | + | - |
| 11 | Carrera | F | - | + | + |

G= good; F= Fair; += marker is present; - = marker is absent.

Table 2. Total $F_2$ plants and $F_3$ families from single crosses and total $F_1$ plants and $F_{1:3}$ families from three-way and double-crosses for marker and lodging evaluation

| Populations | Cross | No. of $F_2$ plants | No. of $F_3$ families |
|---|---|---|---|
| Bi-parental | | | |
| 1 | Carrera/DS Dominator | 86 | 36 |
| 2 | Carrera/Carneval | 96 | 47 |
| 3 | Carrera/Toledo | 98 | na |
| 4 | Carrera/Nitouche | 75 | na |
| 5 | Carrera/Swing | 88 | 50 |
| 6 | Carrera/DS Admiral | 83 | 43 |
| 7 | Carrera/Integra | 80 | 42 |
| 8 | Carrera/Miami | 101 | 73 |
| 9 | Carrera/Majoret | 72 | 45 |
| 10 | Carrera/MP1101 | 78 | 66 |
| Populations | Cross | No. of $F_1$ plants | No. of $F_3$ families |
| Three-way crosses | | | |
| 11 | Carrera/Swing ($F_1$)//CDC April | 34 | 95 |
| 12 | Carrera/Carneval ($F_1$)//CDC April | 24 | 99 |
| 13 | Carrera/DS Admiral ($F_1$)//CDC Minuet | 19 | 90 |
| 14 | Carrera/MP1101 ($F_1$)//CDC Minuet | 37 | 99 |
| 15 | Carrera/Nitouche ($F_1$)//CDC Vienna | 30 | 128 |
| 16 | Carrera/Integra ($F_1$)//CDC Vienna | 21 | 90 |
| Double crosses | | | |
| 17 | Carrera/Majoret ($F_1$)//Carrera/Toledo ($F_1$) | 45 | 81 |
| 18 | Carrera/Toledo ($F_1$)//Carrera/Integra ($F_1$) | 32 | 92 |
| 19 | Carrera/Miami ($F_1$)//Carrera/DS Admiral ($F_1$) | 50 | 85 |
| 20 | Carrera/DS Dominator (F1)//Carrera/Carneval ($F_1$) | 22 | 79 |

**DNA Extraction, PCR amplification and marker scoring**: DNA was extracted using DNAeasy Extraction kit (Qiagen, California). PCR was done in a total volume of 25 µl containing 10 mM TRIS-Cl (pH 8.8), 50 mM KCl, 1.5 mM MgCl2, 200 µM of each of dNTPs, 10 pmol of forward and reverse primers, 50 ng of pea genomic DNA and 1 U *Taq* DNA polymerase (Life Technology). The sequences of the primers that were used to generate the markers are as follows: A001 (Forward: 5'-cttcaccatccatagtgtcg-3'; Reverse: 5'-cacttgcgttccttgtgtg-3'), A002 (Forward: 5'-caaacaatgaaactccggtg-3'; Reverse: 5'-

gcagccaatcaaacacatc-3') and A004 (Forward: 5'-gcgcatgaaatctaggtttg-3'; Reverse: 5'-cacaagaacgaagaacatcg-3'). Amplification was done using a MJ Thermocycler which included a 3 min initial denaturation step at 94 °C followed by 35 cycles at 94 °C for 1 min, a 30s annealing at 58 °C and a 1 min elongation at 72 °C. The PCR products were loaded onto a 1.5 % agarose gel to separate the bands. The bands were visualized and recorded using a Gel-Doc system. The presence and absence of the markers was recorded for each individual line.

**Marker-assisted selection:** The schematics of MAS for the $F_2$ and $F_1$-derived populations are described in Fig. 1 and Fig. 2, respectively. The $F_1$ progeny from single crosses (population 1–10) were selfed to produce $F_2$ seeds. The $F_2$ seeds from each cross were space-planted in four-row plots in the field at Saskatoon, Saskatchewan in 2002. DNA was extracted from leaf tissue of individual $F_2$ plants and scored for the presence or absence of A001 and A004 markers. The $F_2$ plants from each cross were grouped into four classes (T1, T2, T3 and T4) based on a combination of A001 and A004 marker scores (Table 3 and 5). Seeds from each $F_2$ plant were harvested and bulked to generate $F_{2:3}$ families (approximately 40 seeds per family) that were used for lodging evaluation in the field in 2003 (Fig. 1). Other families, which had less than 40 seeds, were omitted from the lodging evaluation, since plant stands would have been too thin to effectively assess lodging.

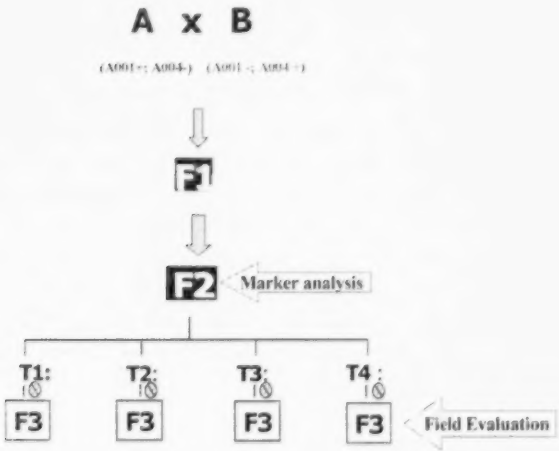


Fig.1. MAS for lodging resistance for the progeny of single crosses (population 1-10)

The $F_1$ seeds from the three-way and double crosses (pop. 11-20) were also space-planted in the field at Saskatoon in 2002. DNA was extracted from leaf tissue of individual $F_1$ plants followed by scoring for the presence or absence of A001 and A004 markers. The $F_1$ plants from each cross were grouped into four classes based on a combination of A001 and A004 marker scores. Two plants from each marker class and cross were selected. The seeds from the selected $F_1$ plants were planted in 5-gallon pots (5 seeds per pot) in a greenhouse in the winter of 2003. The number of $F_2$ seeds that were planted from each of the selected $F_1$ plants was determined based on their marker classes, which were 48 seeds

per plant of T1 class; 24 seeds per plant from each of T2 and T3 class, and 12 seeds per plant from T4 class. DNA was collected from individual $F_2$ plants and scored for the presence or absence of A001 and A004 markers for T1, A001 marker for T2 and A004 marker for T3. No marker scoring was done on plants from T4. The $F_2$ plants from each population were again classified based on their marker scores. Seeds from individual plants that had marker scores of A001(+)A004(+) from T1, A001(+)A004(-) from T2, A001(-)A004(+) from T3 and from all the surviving individual plants of T4 were harvested and bulked to generate $F_{2:3}$ families (Fig. 2).

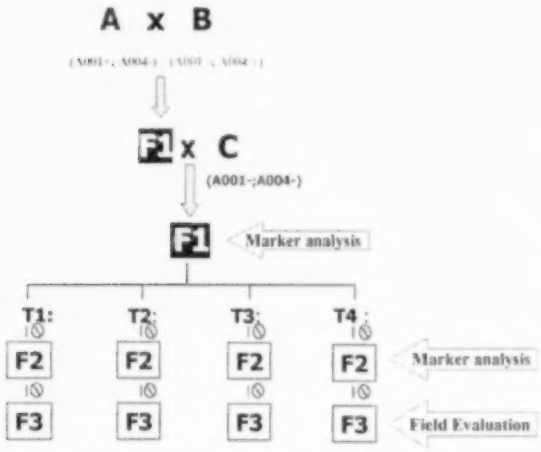


Fig.2. MAS for lodging resistance for the progeny of three-way and double crosses (population 11-20)

Three additional populations, from cross no 12, 13 and 19, were developed without marker assessment to produce $F_3$ families. These populations were designated as unselected 1, 2 and 3, respectively. Because of seed limitation we were only able to generate these three populations for unselected controls. These families were used as comparison for testing the efficiency of MAS for lodging.

**Lodging evaluation and data analysis:** The $F_{2:3}$ families from the 23 populations were planted at the Canada-Saskatchewan Irrigation Diversification Centre (CSIDC) in Outlook, Saskatchewan in the summer of 2003. A completely randomized design with unequal replications was used. The number of replications corresponded with the size of $F_3$ families. The $F_3$ seeds were planted in 3-row (0.8 $m^2$) microplots with 30 cm row spacing and 80 cm between plots in all directions to minimize the interaction between neighboring genotypes. Marker classes were considered the treatment in the experiment. The plots were irrigated using an automatic sprinkler irrigation system. Plot maintenance included fertilizer application based on soil test recommendations and necessary herbicide and insecticide applications to control weeds and aphids. Lodging reaction was assessed at physiological maturity on a plot basis using a 1-9 scale; where 1= upright and 9 = completely lodged. Lodging scores were analyzed separately for each population and compared among the marker classes. Analysis of variance for each population was done using the GLM procedure of the SAS program (SAS Institute, Cary, NC). The

effectiveness of using markers for MAS for lodging resistance was determined by t-test of the differences in lodging scores between pairs of marker classes.

**Fingerprinting of parental lines:** All parental lines used in crossing and commercial pea varieties recommended for production in Saskatchewan blocks were characterized using randomly selected RAPD (random amplified polymorphic DNA), SSR (Simple Sequence Repeats) and ISSR (inverse simple sequence repeats) primers. At least 100 polymorphic bands were generated and scored for each line. A dendrogram showing the relationships among these parental lines was developed based on these marker data. This analysis provides information on the diversity of the lines used as sources of lodging resistance, and will help to draw the overall conclusions from this research. All the commercial pea varieties recommended for production in Saskatchewan were also scored for the markers A001, A002 and A004.

## Results and Discussion

**Marker analysis of $F_1$ and $F_2$ generations:**
A total of 869 $F_2$ plants (ranging from 72 -101 plants per population) derived from ten crosses were scored for the presence or absence of the SCAR markers. Plants derived from all crosses except cross 4 were scored for the A001 and A004 marker. The results of marker analysis for the $F_2$ plants from nine populations of single crosses were summarized in Table 3. Plants from crosses 3 and 4 were also scored for the A002 marker. Chi-square analysis showed that the combination of the A001 and A004 markers followed the segregation of two independent genes (9:3:3:1; $P>0.05$) in eight populations (Table 3), except for population 3 for which the segregation ratio was significantly different from the expected ratio of 9:3:3:1. Figure 3 shows a typical gel photo of the A001 and A004 marker segregation.

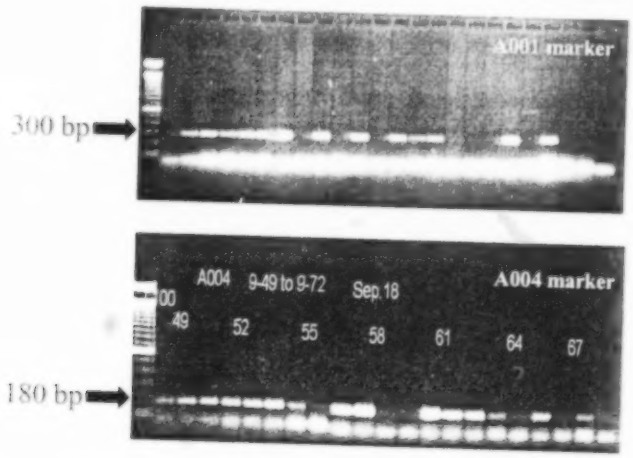


Fig. 3. Examples of the segregation of A001 and A004 markers on the $F_2$ progeny

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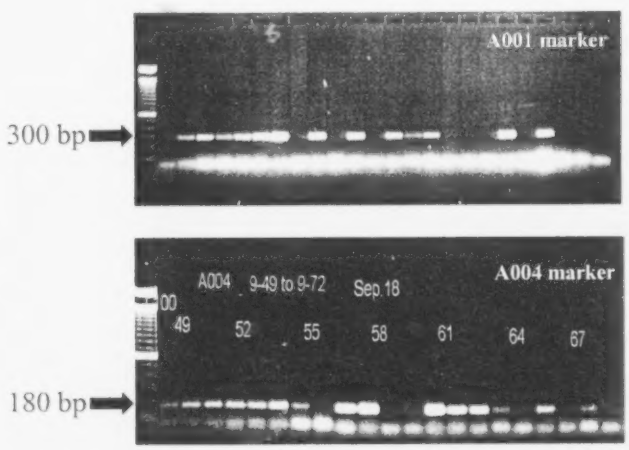


Fig. 3. Examples of the segregation of A001 and A004 markers on the $F_2$ progeny

Table 3. $\chi^2$ analysis of the observed segregation ratio against the expected ratio of 9:3:3:1 of A001 and A004 marker combinations in $F_2$ plants of single crosses

| Population | T1: A001(+) A004(+) | T2: A001(+) A004(-) | T3: A001(-) A004(+) | T4: A001(-) A004(-) | Total | $\chi^2$ (9:3:3:1) | *P* value |
|---|---|---|---|---|---|---|---|
| 1 | 46 | 19 | 19 | 2 | 86 | 3.26 | >0.50 |
| 2 | 50 | 19 | 23 | 4 | 96 | 2.41 | >0.50 |
| 3 | 43 | 25 | 25 | 5 | 98 | 7.6 | <0.05 |
| 5 | 47 | 19 | 16 | 2 | 88 | 2.75 | >0.50 |
| 6 | 44 | 19 | 19 | 1 | 83 | 5.05 | >0.30 |
| 7 | 41 | 15 | 21 | 3 | 80 | 3.6 | >0.40 |
| 8 | 54 | 22 | 21 | 4 | 101 | 1.71 | >0.60 |
| 9 | 41 | 19 | 11 | 1 | 72 | 5.43 | >0.30 |
| 10 | 44 | 13 | 19 | 2 | 78 | 3.19 | >0.50 |

For population 3 and 4, the *P*-values for the independent segregation of the A001 and A002 markers were 0.3 and 0.1, respectively. However, since the A001 and A002 markers were linked at 5.5 cM in the RILs derived from MP1401 × Carneval (Tar'an et al. 2003), further $\chi^2$ tests were done for population 3 and 4. Assuming the genetic distance between A001 and A002 was similar to that in the RIL population derived from MP1401 × Carneval (5.5 cM); the *P*-values for the linked gene segregation model were 0.7 and 0.5 (Table 4), respectively. Thus, the probability for the linkage of A001 and A002 was greater than the probability for their independent segregation in populations 3 and 4.

Table 4. $\chi^2$ analysis of the observed segregation ratio of A001 and A002 markers for population 3 and 4 against the expected ratio of 0.5:0.249: 0.249:0.00063 considering markers are linked at 5.5 cM

| Population | A001(+) A002(+) | A001(+) A002(-) | A001(-) A002(+) | A001(-) A002(-) | Total | $\chi^2$ | *P* value |
|---|---|---|---|---|---|---|---|
| 3 | 13 | 7 | 4 | 0 | 24 | 0.93 | >0.70 |
| 4 | 44 | 16 | 15 | 0 | 75 | 2.33 | >0.50 |

A total of 314 $F_1$ plants derived from three-way and double crosses were also analyzed using the SCAR markers in similar fashion as for the plants derived from single crosses. The plants from populations 11, 12, 13, 14, 16, 19 and 20 segregated for A001 and A004 markers, whereas plants from population 17 and 18 also segregated for A002 marker. The $F_1$ plants from population 15 only segregated for A001 and A002 markers. Chi-square analyses on the A001 and A004 marker combinations demonstrated that the segregation ratio of both markers in all populations except population 15 followed a two independent gene model (Table 5). The segregation of A001 and A002 markers in the $F_1$ plants of population 15 followed a linked gene model at a distance of ~ 10 cM. Segregation analysis of the markers in the $F_1$ plants derived from three-way and double

crosses also supported the two independent marker model, whereas A001 and A002 markers remained linked.

Table 5. $\chi^2$ analyses of the observed segregation ratio of A001 and A004 marker combinations against the expected ratio of 1:1:1:1 for $F_1$ plants derived from three-way crosses (population 11-16) or 9:3:3:1 for $F_1$ plants derived from double crosses (population 17-20)

| Population | T1: A001(+) A004(+) | T2: A001(+) A004(-) | T3: A001(-) A004(+) | T4: A001(-) A004(-) | Total | $\chi^2$ | *P* value |
|---|---|---|---|---|---|---|---|
| 11 | 10 | 8 | 9 | 7 | 34 | 0.59 | >0.80 |
| 12 | 7 | 7 | 6 | 4 | 24 | 1.00 | >0.80 |
| 13 | 6 | 3 | 4 | 6 | 19 | 1.42 | >0.50 |
| 14 | 11 | 9 | 10 | 7 | 37 | 0.95 | >0.80 |
| 16 | 7 | 4 | 5 | 5 | 21 | 0.90 | >0.80 |
| 17 | 25 | 7 | 6 | 7 | 45 | 7.20 | >0.05 |
| 18 | 19 | 7 | 4 | 2 | 32 | 0.89 | >0.80 |
| 19 | 26 | 10 | 12 | 2 | 50 | 1.34 | >0.50 |
| 20 | 11 | 7 | 2 | 2 | 22 | 3.53 | >0.20 |

Note: For population 17 and 18 the data were pooled based on A001 and A004 marker scores only

**Lodging evaluation in $F_1$- and $F_2$-derived $F_3$ families:** Lodging scores of the parental lines and $F_3$ microplots were assessed twice during the growing season. The first assessment was before physiological maturity and the second assessment was at physiological maturity using a 1-9 scale where 1 = completely upright and 9 = completely lodged (Table 6). Since the differences between the lodging scores of the susceptible and resistant parents were greater at the second assessment than at the first assessment, the lodging scores of the second assessment were used in the data analyses. Data were analyzed separately for each population and compared among the marker classes.

Table 6. Lodging scale used in the assessment of pea micro plots

| Lodging scale | Lodging development |
|---|---|
| 1 | Main stems strictly upright |
| 2 | Main stems incline slightly |
| 3 | Main stems at 60° angle |
| 4 | Main stems at 45° angle |
| 5 | Main stems at 30° angle |
| 6 | 1/2 of the main stems flat |
| 7 | 2/3 of the main stems flat |
| 8 | 4/5 of the main stems flat |
| 9 | All main stems flat |

The mean lodging score of the susceptible parents of each population varied from 4.9 to 6.0, while the mean lodging score of the resistant parents varied from 3.0 to 4.2 (Table 7). Assuming that all the parental lines were homozygous, variability within the trial was relatively low as indicated by standard errors.

Table 7. Parental lines, A001, A002 and A004 marker genotypes and the scores of lodging reaction, vine length, days to flowering and days to maturity based on 2003 field trial at Outlook, SK.

| Cultivar | A001 | A002 | A004 | Lodging score (± Se) | Vine length (± Se) | Days to flowering (± Se) | Days to maturity (± Se) |
|---|---|---|---|---|---|---|---|
| Carneval | + | + | - | 3.8 (0.4) | 50 (4) | 51 (1) | 78 (2) |
| Carrera | - | + | + | 6.0 (0.6) | 40 (5) | 48 (2) | 78 (1) |
| CDC April | - | - | - | 4.9 (0.7) | 44 (5) | 54 (2) | 83 (1) |
| CDC Minuet | - | + | - | 5.2 (0.7) | 60 (3) | 52 (2) | 82 (1) |
| CDC Vienna | - | - | - | 5.1 (0.8) | 59 (4) | 53 (1) | 82 (2) |
| DS Admiral | + | + | - | 3.6 (0.8) | 53 (3) | 47 (1) | 79 (1) |
| DS Dominator | + | + | - | 3.7 (0.7) | 56 (3) | 53 (1) | 83 (1) |
| Integra | + | + | - | 4.0 (0.4) | 52 (2) | 46 (1) | 79 (2) |
| Majoret | + | + | - | 3.9 (0.4) | 54 (3) | 48 (1) | 79 (2) |
| Miami | + | + | - | 3.0 (0.7) | 57 (2) | 48 (1) | 78 (1) |
| MP1101 | + | + | - | 3.5 (0.5) | 49 (3) | 51 (1) | 81 (2) |
| Nitouche | + | - | + | 3.7 (0.5) | 53 (2) | 46 (1) | 80 (1) |
| Swing | + | + | - | 3.6 (0.7) | 48 (2) | 46 (1) | 77 (1) |
| Toledo | + | - | - | 4.2 (0.5) | 51 (2) | 45 (1) | 78 (2) |

+ = marker is present; - = marker is absent

The mean lodging score of parents and marker classes in $F_{2:3}$ families for the combination of the presence or absence of A001 and A004 markers revealed a similar trend in all populations which was as follows: susceptible parent > T3 > T4 ≅ T1> T2 > resistant parent (Table 7, 8 and 9). This trend supported the initial hypothesis that there are at least two loci (tagged by A001 and A004 markers) associated with lodging resistance in the pea genome. Plants in T2 class have the resistance alleles at both loci, whereas plants from the T3 class have none of the alleles present. For the populations derived from single crosses, the mean lodging score of T2 class varied from 3.4 to 5.1, while the mean lodging score of T3 class varied from 4.6 to 5.9 across the eight populations. The T2 class for the populations derived from three-way and double crosses varied from 3.5 to 4.3, whereas the T3 class varied from 4.5 to 6.3. T-tests showed significant differences ($P<0.05$) in mean lodging scores between T2 and T3 classes across all populations, except population 9 (Table 10). Larger differences in lodging score were obtained from the combination of A001 and A004 markers than from using single markers alone in all populations assessed. Therefore, using the combination of both markers was more effective than using the individual markers in MAS. The mean vine length varied

from 48 to 57 cm across the eight populations derived from single crosses, and from 48 to 68 cm in the 10 populations derived from three-way and double crosses. The mean number of days to flowering varied from 45 to 55 days across all the populations. The mean number of days to maturity varied from 74 to 81 days across all the populations. For all traits, the mean value for each population was generally within the range of the corresponding parents' values.

Population 15, 17 and 18 segregated for all three markers (A001, A002 and A004). In these populations, when A001 was present, the addition of A002 marker did not significantly affect the expression of the resistance to lodging. For example, in population 15 the mean lodging score of A001(+)A002(+)A004(+) class was 4.3 which was not significantly different ($P < 0.05$) from the mean lodging score of A001(+)A002(-) A004(+) class (4.4). The same trend was also found for populations 17 and 18. These results support the hypothesis A001 and A002 were linked to the same QTL for lodging resistance on LGIII.

Table 8. Mean lodging scores, vine length, days to flowering and days to maturity from different combination of A001 and A004 markers in $F_3$ families of eight populations derived from single crosses

| Marker class | Sample size | Lodging | Vine length | Days to flowering | Days to maturity |
|---|---|---|---|---|---|
| Population 1 | | | | | |
| T1: A001(+); A004(+) | 16 | 4.1 | 54 | 49 | 80 |
| T2: A001 (+); A004(-) | 12 | 3.4 | 55 | 50 | 80 |
| T3: A001(-); A004(+) | 8 | 4.6 | 54 | 49 | 81 |
| T4: A001(-); A004(-) | 0 | na | na | na | na |
| Total | 36 | | | | |
| Population 2 | | | | | |
| T1: A001(+); A004(+) | 27 | 4.6 | 54 | 48 | 76 |
| T2: A001 (+); A004(-) | 7 | 3.8 | 55 | 48 | 77 |
| T3: A001(-); A004(+) | 12 | 5.3 | 47 | 48 | 76 |
| T4: A001(-); A004(-) | 1 | 4.5 | 45 | 48 | 74 |
| Total | 47 | | | | |
| Population 5 | | | | | |
| T1: A001(+); A004(+) | 23 | 5.1 | 53 | 47 | 78 |
| T2: A001 (+); A004(-) | 13 | 4.8 | 52 | 47 | 78 |
| T3: A001(-); A004(+) | 13 | 5.7 | 49 | 48 | 78 |
| T4: A001(-); A004(-) | 1 | 5.0 | 47 | 47 | 78 |
| Total | 50 | | | | |
| Population 6 | | | | | |
| T1: A001(+); A004(+) | 22 | 5.1 | 60 | 48 | 79 |
| T2: A001 (+); A004(-) | 9 | 4.7 | 61 | 48 | 78 |
| T3: A001(-); A004(+) | 12 | 5.5 | 54 | 48 | 79 |
| T4: A001(-); A004(-) | 0 | Na | na | na | na |
| Total | 43 | | | | |
| Population 7 | | | | | |
| T1: A001(+); A004(+) | 25 | 5.1 | 57 | 46 | 78 |
| T2: A001 (+); A004(-) | 4 | 4.3 | 57 | 45 | 76 |
| T3: A001(-); A004(+) | 13 | 5.9 | 51 | 47 | 78 |

| | | | | | |
|---|---|---|---|---|---|
| T4: A001(-); A004(-) | 0 | Na | na | na | na |
| Total | 42 | | | | |
| Population 8 | | | | | |
| T1: A001(+); A004(+) | 44 | 5.4 | 60 | 47 | 79 |
| T2: A001 (+); A004(-) | 10 | 5.1 | 64 | 47 | 79 |
| T3: A001(-); A004(+) | 17 | 5.9 | 51 | 48 | 80 |
| T4: A001(-); A004(-) | 2 | 5.3 | 49 | 47 | 80 |
| Total | 73 | | | | |
| Population 9 | | | | | |
| T1: A001(+); A004(+) | 24 | 5.2 | 52 | 47 | 79 |
| T2: A001 (+); A004(-) | 9 | 4.7 | 58 | 49 | 80 |
| T3: A001(-); A004(+) | 12 | 5.4 | 48 | 48 | 78 |
| T4: A001(-); A004(-) | 0 | Na | na | na | na |
| Total | 45 | | | | |
| Population 10 | | | | | |
| T1: A001(+); A004(+) | 40 | 5.5 | 49 | 49 | 79 |
| T2: A001 (+); A004(-) | 7 | 4.9 | 55 | 50 | 79 |
| T3: A001(-); A004(+) | 17 | 5.9 | 48 | 48 | 79 |
| T4: A001(-); A004(-) | 2 | 5.3 | 42 | 49 | 77 |
| Total | 66 | | | | |

Table 9. Mean lodging scores, vine length, days to flowering and days to maturity from different combination of A001, A002 and A004 markers in $F_3$ families of ten populations derived from three-way and double crosses

| Marker classes | Sample size | Lodging | Vine length | Days to flowering | Days to maturity |
|---|---|---|---|---|---|
| Population 11 | | | | | |
| T1: A001 (+); A004 (+) | 37 | 4.9 | 62 | 53 | 79 |
| T2: A001 (+); A004 (-) | 29 | 3.7 | 48 | 51 | 80 |
| T3: A001 (-); A004 (+) | 18 | 5.2 | 54 | 53 | 80 |
| T4: A001 (-); A004 (-) | 11 | 4.8 | 49 | 55 | 80 |
| Total | 95 | | | | |
| Population 12 | | | | | |
| T1: A001 (+); A004 (+) | 35 | 4.4 | 59 | 53 | 79 |
| T2: A001 (+); A004 (-) | 26 | 3.8 | 57 | 53 | 79 |
| T3: A001 (-); A004 (+) | 28 | 4.9 | 53 | 52 | 79 |
| T4: A001 (-); A004 (-) | 10 | 5.2 | 55 | 52 | 79 |
| Total | 99 | | | | |
| Population 13 | | | | | |
| T1: A001 (+); A004 (+) | 36 | 4.5 | 65 | 51 | 79 |
| T2: A001 (+); A004 (-) | 27 | 3.7 | 67 | 51 | 79 |
| T3: A001 (-); A004 (+) | 17 | 4.7 | 53 | 51 | 79 |
| T4: A001 (-); A004 (-) | 10 | 4.3 | 64 | 51 | 79 |
| Total | 90 | | | | |
| Population 14 | | | | | |
| T1: A001 (+); A004 (+) | 36 | 4.8 | 55 | 52 | 80 |
| T2: A001 (+); A004 (-) | 28 | 3.7 | 57 | 54 | 81 |
| T3: A001 (-); A004 (+) | 20 | 6.3 | 60 | 53 | 80 |

| | | | | | |
|---|---|---|---|---|---|
| T4: A001 (-); A004 (-) | 15 | 4.9 | 60 | 54 | 81 |
| Total | 99 | | | | |
| Population 15 | | | | | |
| A001 (+); A002 (+); A004 (+) | 48 | 4.3 | 64 | 53 | 81 |
| A001 (+); A002 (-); A004 (+) | 19 | 4.4 | 57 | 55 | 81 |
| A001 (+); A002 (+); A004 (-) | 25 | 3.7 | 59 | 53 | 80 |
| A001 (-); A002 (-); A004 (+) | 20 | 5.6 | 50 | 54 | 81 |
| A001 (-); A002 (+); A004 (-) | 16 | 3.8 | 52 | 54 | 80 |
| Total | 128 | | | | |
| Population 16 | | | | | |
| T1: A001 (+); A004 (+) | 36 | 5.1 | 68 | 53 | 81 |
| T2: A001 (+); A004 (-) | 18 | 4.3 | 63 | 53 | 80 |
| T3: A001 (-); A004 (+) | 24 | 5.1 | 64 | 53 | 80 |
| T4: A001 (-); A004 (-) | 12 | 4.8 | 63 | 53 | 80 |
| Total | 90 | | | | |
| Population 17 | | | | | |
| A001 (+); A002 (+); A004 (+) | 27 | 3.8 | 63 | 46 | 79 |
| A001 (+); A002 (-); A004 (+) | 19 | 3.9 | 51 | 46 | 79 |
| A001 (+); A002 (+); A004 (-) | 16 | 3.3 | 50 | 47 | 79 |
| A001 (-); A002 (-); A004 (+) | 19 | 5.8 | 49 | 48 | 79 |
| Total | 81 | | | | |
| Population 18 | | | | | |
| A001 (+); A002 (+); A004 (+) | 20 | 4.1 | 59 | 48 | 80 |
| A001 (+); A002 (-); A004 (+) | 17 | 4.0 | 57 | 47 | 79 |
| A001 (+); A002 (+); A004 (-) | 26 | 3.5 | 67 | 45 | 79 |
| A001 (-); A002 (-); A004 (+) | 15 | 5.8 | 51 | 47 | 79 |
| A001 (-); A002 (+); A004 (+) | 14 | 4.3 | 57 | 47 | 79 |
| Total | 92 | | | | |
| Population 19 | | | | | |
| T1: A001 (+); A004 (+) | 31 | 3.9 | 56 | 47 | 79 |
| T2: A001 (+); A004 (-) | 23 | 3.8 | 54 | 47 | 78 |
| T3: A001 (-); A004 (+) | 23 | 4.5 | 56 | 48 | 79 |
| T4: A001 (-); A004 (-) | 8 | 4.2 | 57 | 47 | 79 |
| Total | 85 | | | | |
| Population 20 | | | | | |
| T1: A001 (+); A004 (+) | 32 | 3.7 | 51 | 51 | 80 |
| T2: A001 (+); A004 (-) | 16 | 3.5 | 56 | 50 | 79 |
| T3: A001 (-); A004 (+) | 17 | 5.2 | 53 | 47 | 80 |
| T4: A001 (-); A004 (-) | 14 | 4.4 | 58 | 48 | 80 |
| Total | 79 | | | | |

Table 10. T-tests for mean lodging reaction among different classes of A001 and A004 marker combinations across 17 populations derived from single, three-way and double crosses

| Population | T2 vs. T1 | T2 vs. T3 | T2 vs. T4 | Population | T2 vs. T1 | T2 vs. T3 | T2 vs. T4 |
|---|---|---|---|---|---|---|---|
| 1 | ** | ** | - | 11 | ns | ** | * |
| 2 | * | ** | ns | 12 | ns | ** | * |
| 5 | * | ** | ns | 13 | * | ** | ns |
| 6 | ns | ** | - | 14 | ns | ** | * |
| 7 | * | ** | - | 16 | * | ** | ns |
| 8 | ns | * | ns | 19 | ns | * | ns |
| 9 | ns | ns | - | 20 | ns | ** | ** |
| 10 | ns | ** | ns | | | | |

* = significant at 0.05 level; ** = significant at 0.01 level; ns = not significant; - = not determined

**Effectiveness of the A001 and A004 markers for MAS:** The effectiveness of the A001 and A004 markers for MAS for lodging resistance was evidenced by the significant differences in lodging score among marker classes in the $F_3$ families. The results demonstrated that the most lodging resistant families were obtained from T2 class for which both alleles for lodging resistance were present. The highest mean lodging scores were obtained from T3 class for which both alleles for lodging resistance were absent. The mean lodging score for T2 class was significantly less than for T3 class in all populations except population 9. Since the expected frequency of T2 plants in $F_2$ populations from single crosses or $F_1$ generation from double crosses is 3/16 (19%), up to 81% of plants without the desired marker combination could be discarded by using these two markers; whereas for the $F_1$ generation derived from three-way crosses the frequency of T2 plants would be ¼, therefore up to 75 % of the plant could be discarded.

The effectiveness of MAS for the T2 class was also supported by the high proportion of lodging resistant $F_3$ families in this class (Table 11). From the 18 populations derived from single, three-way or double crosses, the proportion of the lodging resistant $F_3$ families in the T2 class ranged from 44% to 75%; whereas much lower proportions of resistant $F_3$ families (ranged from 24% - 33%) was obtained from the unselected populations (Table 11 and Fig. 4).

The mean lodging reaction of the families from the T2 class, however, did not exceed the performance of the corresponding lodging resistant parents. The proportion of lodging resistant families in the T2 class also indicated that around 25 % to 54 % of the families lodged. In the RIL population derived from MP1401 × Carneval from which the markers were developed, the two markers accounted for 59 % of the variability for the lodging reaction (Tar'an et al. 2003). These results suggest that additional unknown factor(s) related to lodging exist which could not be explained by these markers. Furthermore, the A001 marker, which is linked in coupling with the major locus for lodging resistance, is a dominant marker that cannot differentiate between homozygous and heterozygous individuals. Therefore, it is likely that some $F_2$ or $F_1$ plants which were heterozygous with regard to this locus were selected within the T2 class. These could have reduced the effectiveness of MAS.

Table 11. Relative proportion of lodging resistant families (lodging score 1 – 4) from different populations of single, three-way and double crosses selected based on T2 class [A001(+) A004(-)] as well as from three unselected populations

| Population | Proportion of lodging resistant | Population | Proportion of lodging resistant |
|---|---|---|---|
| 1 | 9/12 (75 %) | 12 | 12/26 (46 %) |
| 2 | 5/7 (71 %) | 13 | 15/27 (55 %) |
| 5 | 8/13 (61 %) | 14 | 18/28 (64 %) |
| 6 | 5/9 (55 %) | 15* | 16/25 (64 %) |
| 7 | 3/4 (75 %) | 16 | 13/18 (72 %) |
| 8 | 6/10 (60 %) | 17* | 9/16 (56 %) |
| 9 | 6/9 (67 %) | 18* | 17/26 (65 %) |
| 10 | 5/7 (71 %) | 19 | 14/23 (61 %) |
| 11 | 17/29 (59 %) | 20 | 7/16 (44 %) |

| Population | Proportion of lodging resistant |
|---|---|
| Unselected 1 | 39/131 (24 %) |
| Unselected 2 | 31/93 (33 %) |
| Unselected 3 | 23/94 (24 %) |

* For populations 15, 17 and 18 only $F_3$ families with A001(+) and A004(-) were included in the analysis.

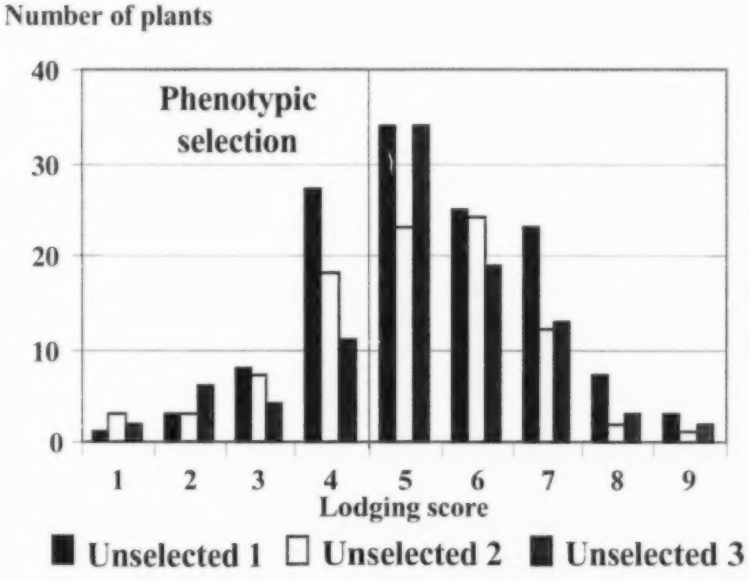

Figure 4. Distribution of $F_3$ families from three unselected populations based on their lodging score in the 2003 field trial at Outlook, SK. Lodging score of 4 (vertical line) was used as the threshold value for phenotypic selection for lodging resistance.

In general, the average lodging score of the parental varieties was lower than the typical lodging score of the same varieties at Outlook. The lodging trial was performed under irrigation to provide favorable conditions for the expression of lodging. However, lodging differences between susceptible and resistant parents were not as great as expected. A potential explanation could be that the plots were lacking nitrogen at the pod-filling stage of the season. Although a soil test had indicated that N was sufficient at the time of planting, it may have been leached out during 11 irrigations during the growing season in 2003, and no top-dressed N was added. As a result, the pea plots were not as vigorous as they could have been, and lodging was not expressed as obviously as expected under ideal conditions. For instance, under similar irrigated conditions at Outlook in 2001, the vine length of Carrera was 65 to 70 cm and its lodging score was 7, whereas in the current trial, the average vine length of Carrera was 40 cm and the average lodging score was 6. Another abiotic stress affecting plant growth and lodging expression was the high temperature during the stage from flowering to pod filling. Lodging is usually correlated with vine length and the weight of pods at physiological maturity and the growing conditions at the pod-filling stage are critical to lodging expression. Due to sub-optimal physiological growth, the yield of Carrera (1540 kg/ha) was also lower than average (approximately 4000 kg/ha) under irrigated conditions at Outlook. In the current trial, the reduced vine length and below average yield were probably the major reasons for the sub-optimal expression of lodging.

**Efficiency of using markers for MAS:** The consumable cost of conducting marker analysis for MAS is approximately $2 per sample. Approximately 200 samples could be analyzed in one day by one technician at a cost of approximately $160 in labour. Thus, the total cost per sample is $2.8. The cost of evaluating one $F_3$ microplot is approximately $10. Thus, if MAS allows for the discarding of undesirable marker classes in $F_1$ or $F_2$, an overall saving to the breeding program should be realized.

**Diversity analysis of parental lines:** The result from molecular marker-based Unweighted pair-group method arithmetic average (UPGMA) cluster analysis is presented in Fig. 5. The correlation coefficient between the cophenetic values of the tree matrix and the genetic similarity matrix, as a measure of the goodness of fit of the cluster was 0.84 corresponding to a good fit. The cluster analysis grouped all the wild *Pisum* accessions separately from the cultivated varieties. By truncating the dendrogram at the similarity value of 0.72, five groups of lodging resistant varieties were identified. The largest group contained seven lodging resistant varieties: Eiffel, Nitouche, Eclipse, Integra, Swing, Toledo and SW Bravo. The second group included DS Admiral, Miami and DS Dominator. Majoret and MP1101 were separated from the rest of the lodging resistant varieties and belong to groups three and five, respectively. Three varieties (Carneval, Logan and Espace) were clustered together in group four. These results indicated that there is sufficient genetic diversity among different groups of lodging resistant varieties. Future breeding for lodging resistance in pea may use varieties from different groups (instead of from a single group) as sources of resistance.

**The utility of A001, A002 and A004 markers on 53 pea cultivars:** A survey of 53 pea cultivars recommended for production in Saskatchewan was conducted using the three markers linked to lodging resistance (Table 12). This analysis indicated that the A001 marker was present in 15 out of 16 pea cultivars with 'good' lodging resistance, and absent in 20 out of 37 cultivars rated as 'fair' or 'poor' for lodging resistance. The A004 marker was absent in 12 out of 16 cultivars with 'good' lodging resistance and present in 18 out of 37 cultivars with 'fair' or 'poor' lodging resistance. The A002 marker was present in 12 out of 16 cultivars with 'good' lodging resistance and absent in 12 out of 37 cultivars with 'fair' or 'poor' lodging resistance. In total, the presence or absence of A001, A004 and A002 markers was consistent with lodging performances in 66%, 57% and 45% of assessed cultivars, respectively. The A002 marker was present more often in cultivars with fair or poor lodging resistance than in cultivars with good lodging resistance. The A001 and A002 markers were only present or absent simultaneously in 34 out of 53 cultivars, equaling 64% of the total number of cultivars. In the other 19 cultivars, one marker was present, while the other was absent. The diversity analysis among the 53 pea cultivars indicated that the lodging resistant cultivars had relatively diverse genetic background. Therefore, these results suggest that A001 and A004 markers may have a broad application for pre-screening parents and MAS for the progeny in breeding for lodging resistance in pea.

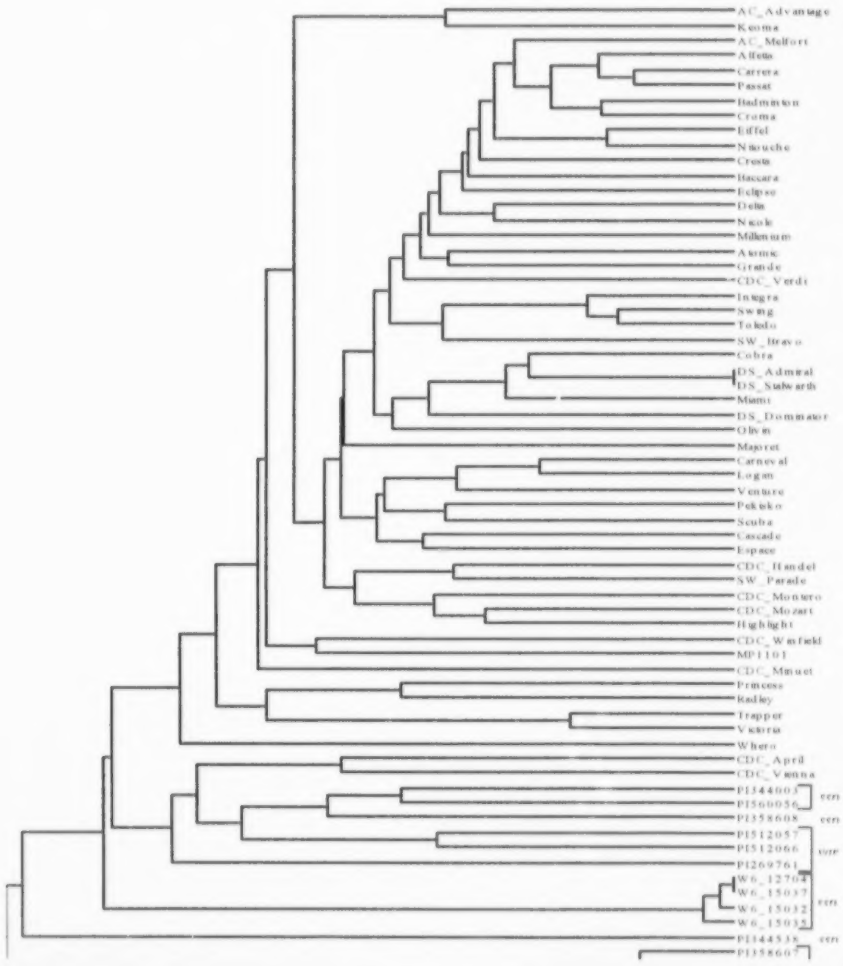

Figure 5. Dendrogram for 53 pea varieties and 21 wild *Pisum* accessions based on a cluster analysis (UPGMA) of genetic similarity estimates (Dice similarity coefficient) from RAPD, SSR and ISSR data.

Table 12. Relative lodging reaction and the scores of A001, A002 and A004 markers for 53 pea cultivars recommended for production in Saskatchewan

| Cultivar | Lodging | A001 | A002 | A004 | Cultivar | Lodging | A001 | A002 | A004 |
|---|---|---|---|---|---|---|---|---|---|
| AC Melfort | F | - | + | + | Grande | F | - | - | + |
| Alfetta | F | - | + | + | SW Parade | F | + | + | - |
| Atomic | F | + | - | - | Venture | F | + | + | - |
| Baccara | F | - | - | + | AC Advantage | P | - | + | + |
| Badminton | F | - | - | + | Keoma | P | + | - | + |
| **Carrera** | F | - | + | + | Olivin | P | + | + | - |
| Cascade | F | + | + | - | Princess | P | + | + | - |
| **CDC April** | F | - | - | - | Trapper | P | - | + | - |
| CDC Handel | F | + | + | + | Victoria | P | - | - | - |
| **CDC Minuet** | F | - | + | - | Whero | P | - | + | + |
| CDC Montero | F | + | + | - | **Carneval** | G | + | + | - |
| CDC Mozart | F | + | + | - | DS 4931 | G | + | + | - |
| CDC Verdi | F | + | + | - | **DS Admiral** | G | + | + | - |
| **CDC Vienna** | F | - | - | - | **DS Dominator** | G | + | + | - |
| CDC Winfield | F | - | + | - | Eclipse | G | - | - | + |
| Cobra | F | + | + | + | Eiffel | G | + | - | - |
| Cresta | F | - | - | + | Espace | G | + | + | + |
| Croma | F | - | + | + | **Integra** | G | + | + | - |
| Delta | F | + | + | + | Logan | G | + | + | - |
| DS Stalwarth | F | + | + | - | **Majoret** | G | + | + | - |
| Highlight | F | + | + | - | **Miami** | G | + | + | - |
| Millenium | F | - | + | + | **MP1101** | G | + | + | - |
| Nicole | F | - | + | + | **Nitouche** | G | + | - | + |
| Passat | F | - | + | + | SW Bravo | G | + | + | + |
| Pekisko | F | + | - | - | **Swing** | G | + | + | - |
| Radley | F | + | - | - | **Toledo** | G | + | - | - |
| Scuba | F | + | + | + | | | | | |

Lodging resistance ratings: G=good, F=fair, P=poor; += marker is present; - = marker is absent;
Bold indicates the cultivars used as parents in this project.

**Conclusion:** The results of the current study confirmed the presence of at least two loci associated with lodging resistance in pea. Using markers linked to each locus, we were able to differentiate the individuals carrying different loci for lodging resistance. The lowest lodging scores for each population derived from single, three-way and double crosses were obtained from T2 marker class [A001(+)A004(-)]. A higher proportion of

lodging resistant $F_3$ families was obtained from T2 class as compared to conventional phenotypic selection for lodging resistance. The current cost estimate demonstrated a cheaper cost for MAS than phenotypic selection for lodging resistance using microplots at the $F_3$ generation. Thus, the current research demonstrated that A001 and A004 are useful for MAS for lodging resistance in early generations of pea breeding.

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**Papers/Presentations:**

Tar'an, B.,C. Zhang, T. Warkentin, A. Tullu and A. Vandenberg. 2004. Genetic Diversity Among Varieties and Wild Species Accessions of Pea (*Pisum sativum* L.) Based on Molecular Markers and Morphological/physiological characters. Genome (accepted)

T.D. Warkentin, B. Tar'an, C. Zhang, K. Bett, A. Tullu, D. Somers, and A. Vandenberg, 2004. Marker-assisted Selection for Lodging Resistance in Pea. A. Schneider, (ed.), Proceedings 5th European Conference on Grain Legumes (Dijon, France).

Zhang, C., Tar'an, B., and Warkentin, T. D. (2003) Implementation of marker-assisted selection for lodging resistance in pea breeding:

~~This poster was presented at~~:

- Soils and Crops 2003. Extension Division, University of Saskatchewan (Saskatoon) (best graduate student poster)
- Pulse Days 2003, Saskatchewan Pulse Growers (Saskatoon)
- 4th Canadian Pulse Research Workshop 2003 (Edmonton)

Information of benefit to producers, processors, or governments:

Implementation of marker assisted selection for lodging resistance in pea breeding will lead to the release of cultivars with improved lodging resistance. In addition, utilization of markers for lodging resistance will result in the discarding of lodging susceptible progeny in the early phase of the breeding process, allowing more stringent selection for other traits of interest, including resistance to mycosphaerella blight and improved quality for food and feed.

(d) **Personnel:**

Dr. Bunyamin Tar'an supervised the day-to-day progress of this research project.

Mr. Chunzhen Zhang conducted the single cross aspects of this study as the major portion of his MSc research project in the Department of Plant Sciences, University of Saskatchewan.

**(e) Equipment purchased:**
None

**(f) Project Developed Materials:**
None

**(g) Project Photos:**
Numerous gel photos have been taken in the SCAR marker assessment of parental lines. Representative photos were included in presentations and manuscripts arising from this research and are available on request.

**(h) Acknowledgement:**
The Saskatchewan Agricultural Development Fund has been and will be acknowledged in all presentations where this research project is mentioned.

**(i)Expense Statement:**
Will be provided.

**(j) ICAR Data Entry**
Submitted.